

Figure 1
Interleukin-21

1 GGCACGAGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCT 60
1 A R V D T D E D R Y P Q K L A F A E C L 20
Domain I Domain II

61 GTGCAGAGGCTGTATCGATGCACGGACGGGCGCGAGACAGCTGGCCTCAACTCCGTGCG 120
21 C R G C I D A R T G R E T A A L N S V R 40
Domain II

121 GCTGCTCCAGAGCCTGCTGGTGTGCGCCGCGCCCTGCTCCCGGACGGCTCGGGGCT 180
41 L L Q S L L V L R R R P C S R D G S G L 60
Domain III

181 CCCACACCTGGGGCCTTTGCCTTCCACACGAGTTTCATCCACGTCCCCGTGGCTGCAC 240
61 P T P G A F A F H T E F I H V P V G C T 80
Domain IV

241 CTGCGTGTGCCCCGTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAGT 300
81 C V L P R S V 87
Domain IV

301 GTGCTCCCCAGAGGGCACCCCCCTATTTATGTATTATTATTATTATATGCTCCCC 360

361 AACACTACCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGACAGCCCCCACTGTTCCTC 420

421 CTCATCTCCAGCCTCAGTAGTTGGGGGTGAAGGAGCTCAGCACCTCTTCCAGCCCTTAA 480

481 AGCTGCAGAAAAGGTGTACACGGCTGCCTGTACCTTGGYTCCCTGTCTCTCCCGCT 540

541 TCCCTTACCTTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGA 600

601 AGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACAC 660

661 AA 705

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Figure 2A
Interleukin-22

1 GGAATTGGCAGAGCTCGTGCCGTGCTCAGTGCCTTCCACCACAGCTGCAGCTGGGGC 60
1 N S A R A R A V L S A F H H T L Q L G P 20

61 CGCGTGAGCAGGCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCGCGACCGCGCT 120
21 R E Q A R N A S C P A G G R P A D R R F 40

121 TCCGCGCGCCCAACCTGCGCAGCGTGTGCGCCTGGGCCTACAGAATCTCCTACGACC 180
41 R P P T N L R S V S P W A Y R I S Y D P 60
Domain I

181 CGGCGAGGTACCCCAAGTACCTGCCTGAAGCCTACTGCCTGTGCGGGGCTGCCTGACCG 240
61 A R Y P R Y L P E A Y C L C R G C L T G 80
Domain I Domain II

241 GGCTGTTGCGCGAGGAGGACGTGCGCTTCCGAGCGCCCTGTCTACATGCCACCGTCG 300
81 L F G E E D V R F R S A P V Y M P T V V 100
Domain III

301 TCCTGCGCGCACCCCGCCTGCGCGGGCGCGCTTCCGTCTACACCGAGGCCTACGTCA 360
101 L R R T P A C A G G R S V Y T E A Y V T 120
Domain III

361 CCATCCCCGTGGGCTGCACCTGCGTCCCCGAGCGGAGAAGGACGCAGACAGCATCAACT 420
121 I P V G C T C V P E P E K D A D S I N S 140
Domain IV

421 CCAGCATCGACAAACAGGGCGCCAAGCTCCTGCTGGGGCCCAACGACGCGCCGCTGGCC 480
141 S I D K Q G A K L L L G P N D A P A G P 160

481 CCTGAGGCCGGTCTGCCCCGGGAGGTCTCCCCGGCCCGCATCCCGAGGCGCCCAAGCTG 540

541 GAGCCGCTTGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGACCGAGCAAACCAAGTG 600

601 CCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCA 660

661 TCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACC 720

721 CGGCACGGGCATCCTGTGTGCGGCCCGCATGGAGGGTTTGGAAAAGTTACGAGGGCTCC 780

781 CTGAGGAGCCTCTCAGATCGGCTGCTGCGGGTGCAGGGCGTACTCACCGCTGGGTGCTT 840

841 GCCAAAGAGATAGGGACGCATATGCTTTTAAAGCAATCTAAAAATAATAATAAGTATAG 900

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Figure 2B
Interleukin-22

901 CGACTATATACCTACTTTTAAATCAACTGTTTGAATAGAGGCAGAGCTATTTTATATT 960
961 ATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTACTTCTTC 1020
1021 TGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTGTAGCTGGTACACTC 1080
1081 TGGCCTGGGCTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCT 1140
1141 CATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGG 1200
1201 ATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGTTCCAAAGATCTCAGATTGG 1260
1261 TTTAGTCATGAATACATAAACAGTCTCAAAGTGCACAATTTTTCCCCCTTTTGAAAG 1320
1321 CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGAACGTGACATCTTT 1380
1381 GCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG 1440
1441 CTGAATATGAGGACAAAGTGGGCCAGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT 1500
1501 GTTCTGCAATCTGCCACGAGAGCTAGGTCCCTGATCTTTCTTTAGATTGAAAGTCTGT 1560
1561 CTCTGAACACAATTATTTGTAAAAGTTAGTAGTCTTTTAAATCATTAAAAGAGGCTT 1620
1621 GCTGAAAAAAAAAAAAAAAAAAAA 1642

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	10	20	30	40	50	
1	M T P G K T S L V S L	- - - - -	E A I V K A G I T I P R N	P G C P N S E	D - - - -	II-17.aa
1	M S P G R A S S V S L	- - - - -	A A T V K A A I I P Q S S A C P N T E A	- - - - -	- - - - -	mII-17.aa
1	M T F R M T S L V - L	- - - - -	D C I V K S E I T S A Q T P R C L A A N N	- - - - -	- - - - -	vII-17.aa
1	M D W P H N L L F L L	T I S I F L G L G Q P R S P K S K	R K G Q G R P G P L A P	G P H Q V P L D L V	- - - - -	II20.aa
1	A - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	II-21.aa
1	M T L L P G L L F L - -	- - T W L H T C L A H H D P S L R G H P H S H G T P H C Y S A E	- - - - -	- - - - -	- - - - -	II21FL.aa
1	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	II-22.aa
1	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	II22ex

	60	70	80	90	100
39	-	-	-	-	-
41	-	-	-	-	-
38	-	-	-	-	-
51	-	-	-	-	-
2	-	-	-	-	-
48	-	-	-	-	-
5	-	-	-	-	-
12	-	-	-	-	-

Figure 3A

	110	120	130	140	150		
67	- - - - - Y	N R S T S P W	N L H R	N E D P E	R Y P S V	I W E A K C R H L G C I N A D - G N V D Y	IL-17.aa
70	- - - - - L	N R S T S P W	T L H R	N E D P D	R Y P S V	I W E A Q C R H Q R C V N A E - G K L D H	mIL-17.aa
63	- - - - - Y	N R S T S P W	T L H R	N E D Q D	R Y P S V	I W E A K C R Y L G C V N A D - G N V D Y	vIL-17.aa
88	L Q L W M S N K -	R S L S P W	G Y S I N H	D P S R I	P V D L	P E A R C L C L G C V N P F T M Q E D R	IL20.aa
2	- - - - -	- - - - -	- R V D T	D E D R Y	P Q K L	A F A E C L C R G C I D A R T G R E T A	IL-21.aa
96	V - L E A D T H Q	R S I S P W	R Y R V D T	D E D R Y	P Q K L	A F A E C L C R G C I D A R T G R E T A	IL21FL.aa
38	R R F R P P T N L	R S V S P W	A Y R I S Y	D P A R Y	P R Y L	P E A Y C L C R G C L T G L F G E E D V	IL-22.aa
1	R R F R P P T N L	R S V S P W	A Y R I S Y	D P A R Y	P R Y L	P E A Y C L C R G C L T G L F G E E D V	IL22ext.aa

	160	170	180	190	200	
1109	H M N S V P I Q Q E I L V L R R E P - - - - - P H C P N S F R L E K I L - - V S V G C T C V T P I L-17.aa					
1112	H M N S V L I Q Q E I L V L K R E P - - - - - E S C P F T F R V E K M L - - V G V G C T C V A S mIL-17.aa					
1105	H M N S V P I Q Q E I L V V R K G H - - - - - Q P C P N S F R L E K M L - - V T V G C T C V T P vIL-17.aa					
1137	S M V S V P V F - S Q V P V R R R L C P P P P R T G P C R Q - - - R A V M E T I A V G C T C I - - I L20.aa					
335	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - I L-21.aa					
1145	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - I L21FL.aa					
88	R F R S A P V Y M P T V L R R T P A C A G R S V - - - - - Y T E A Y V T I P V G C T C V P E I L-22.aa					
101	R F R S A P V Y M P T V L R R T P A C A G R S V - - - - - Y T E A Y V T I P V G C T C V P E I L22ext.aa					

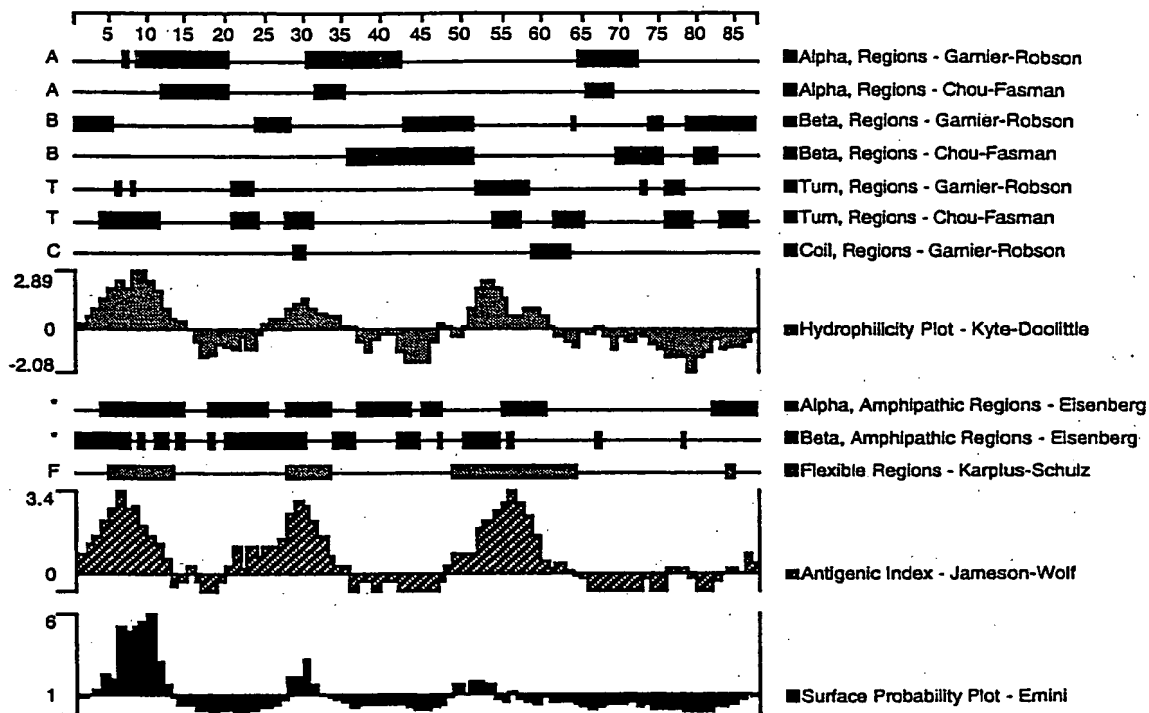
Figure 3B

	210	220	230
150	I V H H V A		
153	I V R Q A A		
146	I V H N V D		
180	- - - - -	- - - - -	- - - F
83	- - - - -	- - - - -	- L P R S V
193	- - - - -	- - - - -	- L P R S V
131	P E K D A D S I N S S I D K Q G A K L L L G P N D A P A G P		
44	P E K D A D S I N S S I D K Q G A K L L L G P N D A P A G P		

IL-17.aa
mIL-17.aa
vIL-17.aa
IL20.aa
IL-21.aa
IL21FL.aa
IL-22.aa
IL22ext

Figure 3C

Figure 4
Interleukin-21 Polypeptide Analysis



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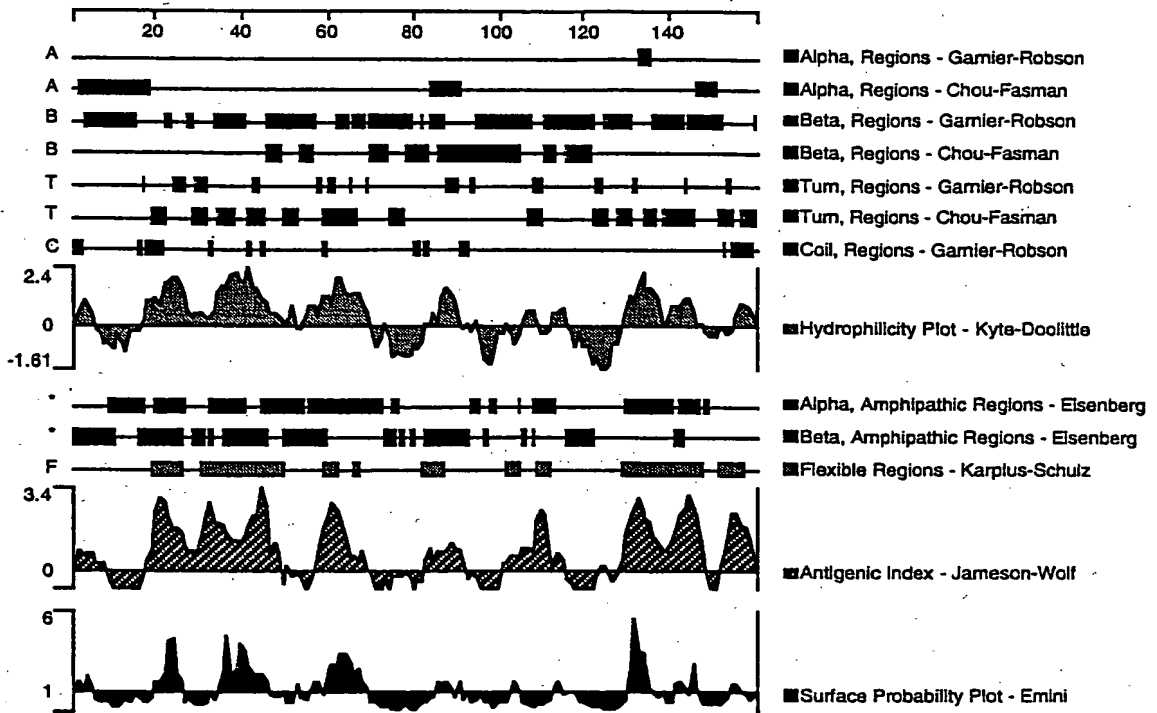


Figure 6A
Interleukin-21

1 GCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCCCGGCCTCCTGTTT 60
1 M T L L P G L L F 9

61 CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCAGCCCCAC 120
10 L T W L H T C L A H H D P S L R G H P H 29

121 AGTCACGGTACCCACACTGCTACTCGGCTGAGGAAGTCCCCCTCGGCCAGGCCCCCCCA 180
30 S H G T P H C Y S A E E L P L G Q A P P 49
Domain V

181 CACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGC 240
50 H L L A R G A K W G Q A L P V A L V S S 69
Domain VI

241 CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGGCCG 300
70 L E A A S H R G R H E R P S A T T Q C P 89

301 GTGCTGGCGCCGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGG 360
90 V L R P E E V L E A D T H Q R S I S P W 109
Domain VII

361 AGATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC 420
110 R Y R V D T D E D R Y P Q K L A F A E C 129
Domain I Domain II

421 CTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG 480
130 L C R G C I D A R T G R E T A A L N S V 149
Domain II

481 CGGCTGCTCCAGAGCCTGCTGGTGTGCGCCGCGGCCCTGCTCCCGCGACGGCTCGGGG 540
150 R L L Q S L L V L R R R P C S R D G S G 169
Domain III

541 CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCGCCGTCGGCTGC 600
170 L P T P G A F A F H T E F I H V P V G C 189
Domain IV

601 ACCTGCGTGTGCCCCGTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAC 660
190 T C V L P R S V 197
Domain IV

661 GTGTGCTCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCC 720

721 CCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTC 780

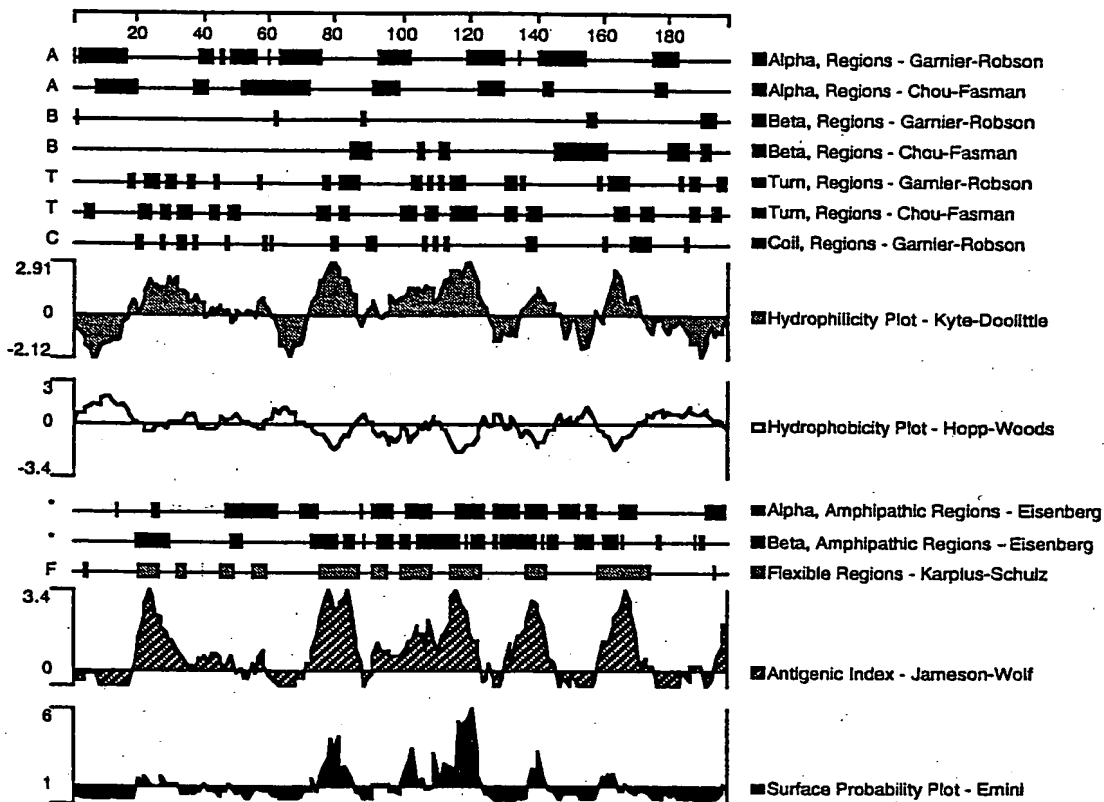
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Figure 6B
Interleukin-21

781 TCCTCATCTCCAGCCTCAGTAGTTGGGGTGAAGGAGCTCAGCACCTCTTCCAGCCCTT 840
841 AAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCTCTGCTCCCGG 900
901 CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960
961 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTATTATTAAACTGATGAAC 1020
1021 AA 1067

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Figure 7
Interleukin-21 Polypeptide Analysis



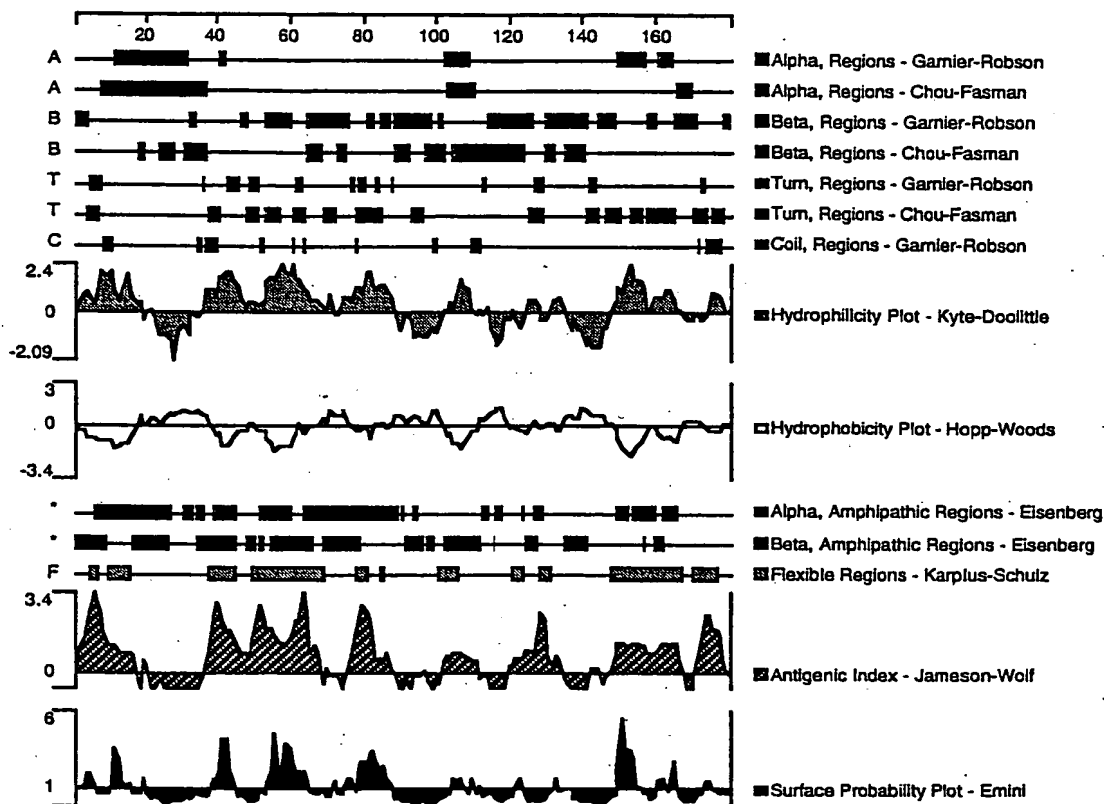
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Figure 8
Interleukin-22

1	GGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGCGCGC	60
1	G C A D R P E E L L E Q L Y G R L A A G	20
	CD-VI	
	#	
61	GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGCGCGCTGAGCAGGCGCGCAACGCG	120
21	<u>V L S A F H H T L Q L G P R E Q A R N A</u>	40
	CD-VI	
121	AGCTGCCCCGCGAGGGGGCAGGCCCGCCGACCGCGCTTCGGCGCGCCACCAACCTGCGC	180
41	<u>S C P A G G R P A D R R F R P P T N L R</u>	60
181	AGCGTGTGCCCCCTGGGCCTACAGAATCTCCTACGACCCGCGAGGTACCCAGGTACCTG	240
61	<u>S V S P W A Y R I S Y D P A R Y P R Y L</u>	80
	CD-VII	CD-I
241	CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCCGGCGAGGAGGACGTG	300
81	<u>P E A Y C L C R G C L T G L F G E E D V</u>	100
	CD-II	
301	CGCTTCGCGAGCGCCCCCTGTCTACATGCCACCGTCGTCTGCGCCGCACCCCGCCTGC	360
101	R F R S A P V Y M P T <u>V V L R R T P A C</u>	120
	CD-III	
361	GCCGCGGCGCGTTCGCTCTACACCGAGGCCTACGTACCATCCCCGTGGGCTGCACCTGC	420
121	<u>A G G R S V Y T E A Y V T I P V G C T C</u>	140
	CD-IV	
	#	
421	GTCCCCGAGCCGAGAAGGACGCGAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC	480
141	<u>V P E P E K D A D S I N S S I D K Q G A</u>	160
	CD-IV	
481	AAGTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGA	522
161	K L L L G P N D A P A G P	174

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Figure 9
Interleukin-22 Polypeptide Analysis



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